

Patent Application US/07/807,043A

#11
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(1) GENERAL INFORMATION:

- (i) APPLICANTS: Boon, Thierry, Van den Eynde, Beno t
- (ii) TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor Rejection Antigens and Uses Thereof
- (iii) NUMBER OF SEQUENCES: 16
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Felfe & Lynch
 - (B) STREET: 805 Third Avenue
 - (C) CITY: New York City
 - (D) STATE: New York
 - (F) ZIP: 10022
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
 - (B) COMPUTER: IBM
 - (C) OPERATING SYSTEM: PC-DOS
 - (D) SOFTWARE: Wordperfect
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: 07/807,043
 - (B) FILING DATE: 12-DECEMBER-1991
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: 07/764,364
 - (B) FILING DATE: 23-SEPTEMBER-1991
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: 07/728,838
 - (B) FILING DATE: 9-JULY-1991
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: 07/705,702
 - (B) FILING DATE: 23-May-1991
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Hanson, Norman D.
 - (B) REGISTRATION NUMBER: 30,946
 - (C) REFERENCE/DOCKET NUMBER: LUD 253.3
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: (212) 688-9200
 - (B) TELEFAX: (212) 838-3884

(2) INFORMATION FOR SEQUENCE ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 462 base pairs
 - (B) TYPE: nucleic acid

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54 (C) STRANDEDNESS: singular
55 (D) TOPOLOGY: linear
56 (ii) MOLECULE TYPE: genomic DNA
57 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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62 ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT GAAGATCCTG 60
63 ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT CAGCCAATGA GCTTACTGTT 120
64 CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG AAGTTTGTCA AGTTCCGCCT ACAGCTCTAG 180
65 CTTGTGAATT TGTACCCCTT CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC 240
66 CCCCCTCCCA CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT 300
67 AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCTTT GCTCTCCAG CATGCATTGT 360
68 GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG CTAGCTTGCG ACTCTACTCT 420
69 TATCTTAACT TAGCTCGGCT TCCTGCTGGT ACCCTTTGTG CC 462
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71
72 (2) INFORMATION FOR SEQUENCE ID NO: 2:
73 (i) SEQUENCE CHARACTERISTICS:
74 (A) LENGTH: 675 base pairs
75 (B) TYPE: nucleic acid
76 (C) STRANDEDNESS: singular
77 (D) TOPOLOGY: linear
78 (ii) MOLECULE TYPE: genomic DNA
79 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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83 Met Ser Asp Asn Lys Lys Pro Asp Lys Ala His Ser Gly Ser Gly Gly
84 5 10 15
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87 Asp Gly Asp Gly Asn Arg Cys Asn Leu Leu His Arg Tyr Ser Leu Glu
88 20 25 30
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90 GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC TTC GCT GTT GTC ACA ACA 144
91 Glu Ile Leu Pro Tyr Leu Gly Trp Leu Val Phe Ala Val Val Thr Thr
92 35 40 45
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94 AGT TTT CTG GCG CTC CAG ATG TTC ATA GAC GCC CTT TAT GAG GAG CAG 192
95 Ser Phe Leu Ala Leu Gln Met Phe Ile Asp Ala Leu Tyr Glu Glu Gln
96 50 55 60
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99 Tyr Glu Arg Asp Val Ala Trp Ile Ala Arg Gln Ser Lys Arg Met Ser
100 65 70 75 80
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102 TCT GTC GAT GAG GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC 288
103 Ser Val Asp Glu Asp Glu Asp Asp Glu Asp Asp Glu Asp Asp Tyr Tyr
104 85 90 95
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106 GAC GAC GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT 336

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111 Glu Glu Glu Glu Leu Glu Asn Leu Met Asp Asp Glu Ser Glu Asp Glu
112      115      120      125
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114 GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA GCT GAG GAA ATG      432
115 Ala Glu Glu Glu Met Ser Val Glu Met Gly Ala Gly Ala Glu Glu Met
116      130      135      140
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118 GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT GGC CAT CAT TTA AGG AAG      480
119 Gly Ala Gly Ala Asn Cys Ala Cys Val Pro Gly His His Leu Arg Lys
120 145      150      155      160
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122 AAT GAA GTG AAG TGT AGG ATG ATT TAT TTC TTC CAC GAC CCT AAT TTC      528
123 Asn Glu Val Lys Cys Arg Met Ile Tyr Phe Phe His Asp Pro Asn Phe
124      165      170      175
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126 CTG GTG TCT ATA CCA GTG AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT      576
127 Leu Val Ser Ile Pro Val Asn Pro Lys Glu Gln Met Glu Cys Arg Cys
128      180      185      190
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130 GAA AAT GCT GAT GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAA GAG      624
131 Glu Asn Ala Asp Glu Glu Val Ala Met Glu Glu Glu Glu Glu Glu Glu
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134 GAG GAG GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT      672
135 Glu Glu Glu Glu Glu Glu Glu Met Gly Asn Pro Asp Gly Phe Ser Pro
136 210      215      220      225
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138 TAG      675
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140 (2) INFORMATION FOR SEQUENCE ID NO: 3:
141 (i) SEQUENCE CHARACTERISTICS:
142 (A) LENGTH: 228 base pairs
143 (B) TYPE: nucleic acid
144 (C) STRANDEDNESS: singular
145 (D) TOPOLOGY: linear
146 (ii) MOLECULE TYPE: genomic DNA
147 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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152 GCATGCAGTT GCAAAGCCCA GAAGAAAGAA ATGGACAGCG GAAGAAGTGG TTGTTTTTTT      60
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159 (2) INFORMATION FOR SEQUENCE ID NO: 4:

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160 (i) SEQUENCE CHARACTERISTICS:
161 (A) LENGTH: 1365 base pairs
162 (B) TYPE: nucleic acid
163 (C) STRANDEDNESS: singular
164 (D) TOPOLOGY: linear
165 (ii) MOLECULE TYPE: genomic DNA
166 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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172 GAAGATCCTG ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTATCCCT 100
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174 AAGTTTGTCA AGTCCGCCT ACAGCTCTAG CTTGTGAATT TGTACCCTTT 200
175 CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCTCCCA 250
176 CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT 300
177 AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCTTT GCTCTCCAG 350
178 CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG 400
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180 ACCCTTTGTG CC 462
181 ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA 504
182 GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG 546
183 TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC 588
184 TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC 630
185 ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC 672
186 TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG 714
187 GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC GAC GAC 756
188 GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT 798
189 GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA 840
190 GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA 882
191 GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GGT GGT GTT CCT 924
192 GGC CAT CAT TTA AGG AAG AAT GAA GTG AAG TGT AGG ATG ATT 966
193 TAT TTC TTC CAC GAC CCT AAT TTC CTG GTG TCT ATA CCA GTG 1008
194 AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT GAA AAT GCT GAT 1050
195 GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAG GAG GAG 1092
196 GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT 1134
197 TAG 1137
198 GCATGCAGTT GCAAAGCCCA GAAGAAAGAA ATGGACAGCG GAAGAAGTGG 1187
199 TTGTTTTTTT TTCCCTTCA TTAATTTTCT AGTTTTTAGT AATCCAGAAA 1237
200 ATTTGATTTT GTTCTAAAGT TCATTATGCA AAGATGTCAC CAACAGACTT 1287
201 CTGACTGCAT GGTGAACTTT CATATGATAC ATAGGATTAC ACTTGTACCT 1337
202 GTTAAAAATA AAAGTTTGAC TTGCATAC 1365
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206 (2) INFORMATION FOR SEQUENCE ID NO: 5:
207 (i) SEQUENCE CHARACTERISTICS:
208 (A) LENGTH: 4698 base pairs
209 (B) TYPE: nucleic acid
210 (C) STRANDEDNESS: singular
211 (D) TOPOLOGY: linear
212 (ii) MOLECULE TYPE: genomic DNA

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213 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
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221 CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCTCCCA 250
222 CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT 300
223 AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCTTT GCTCTCCCAG 350
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226 ACCCTTTGTG CC 462
227 ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA 504
228 GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG 546
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230 TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC 630
231 ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC 672
232 TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG 714
233 GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC GAC GAC 756
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236 GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA 882
237 GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC T 916
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246 TCACCAGCTT TGCTCTCCCT GCTCCCCCTC CCCTTTTGCA CCTTTTCTTT 1366
247 TCCTGCTCCC CTCCCCCTCC CCTCCCTGTT TACCCTTCAC CGCTTTTCCT 1416
248 CTACCTGCTT CCCTCCCCCT TGCTGCTCCC TCCCTATTTG CATTTTCGGG 1466
249 TGCTCCTCCC TCCCCCTCCC CCTCCCTCCC TATTTGCATT TTCGGGTGCT 1516
250 CCTCCCTCCC CCTCCCCAGG CCTTTTTTTT TTTTTTTTTT TTTTTTTTTT 1566
251 TTGGTTTTTC GAGACAGGGT TTCTCTTTGT ATCCCTGGCT GTCCTGGCAC 1616
252 TCACTCTGTA GACCAGGCTG GCCTCAAAC CAGAAATCTG CCTGCCTCTG 1666
253 CCTCCCAAAT GCTGGGATTA AAGGCTTGCA CCAGGACTGC CCCAGTGCAG 1716
254 GCCTTTCTTT TTTCTCCTCT CTGGTCTCCC TAATCCCTTT TCTGCATGTT 1766
255 AACTCCCCTT TTGGCACCTT TCCTTTACAG GACCCCCCTC CCCTCCCCTG 1816
256 TTCCCTTCCG GCACCTTCC TAGCCCTGCT CTGTTCCCTC TCCCTGCTCC 1866
257 CCTCCCCCTC TTTGCTCGAC TTTTAGCAGC CTTACCTCTC CCTGCTTCT 1916
258 GCCCCGTTCC CCTTTTTTGT GCCTTTCCTC CTGGCTCCCC TCCACCTTCC 1966
259 AGCTCACCTT TTTGTTTGTG TGCTTGTGTT GTTGTGTTGTT TTGCTTTTTT 2016
260 TTTTTTTTTT GCACCTTGTG TTCCAAGATC CCCCTCCCCC TCCGGGCTTC 2066
261 CCTCTGTGTG CCTTTCCTGT TCCCTCCCCC TCGCTGGCTC CCCCCTCCCT 2116
262 TCTGCCTTTC CTGTCCCTGC TCCCTTCTCT GCTAACCTTT TAATGCCTTT 2166
263 CTTTTCTAGA CTCCCCCTC CAGGCTTGCT GTTTGCTTCT GTGCACTTTT 2216
264 CCTGACCCTG CTCCCCCTCC CCTCCAGCT CCCCCCTCTT TTCCACCTC 2266
265 CCTTTCTCCA GCCTGTCACC CCTCCTTCTC TCCTCTCTGT TTCTCCCACT 2316

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266 TCCTGCTTCC TTTACCCCTT CCCTCTCCCT ACTCTCCTCC CTGCCTGCTG 2366
267 GACTTCCTCT CCAGCCGCCC AGTTCCCTGC AGTCCTGGAG TCTTTCCTGC 2416
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269 ATGTGTCTCT CTCCTATCT ATCCCTTCCT TTCTGTCCCC TCTCCTCTGT 2516
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272 TCCATGTCCC CTCTCAATTC CCTGTCCCAT TGTGCTCCCT CACATCTTCC 2666
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283 TAGTGATATT TCCCCTAAA AATTATAACA AACAGATTCA TGATTTGAGA 3216
284 TCCTTCTACA GGTGAGAAGT GGAAAAATTG TCACATATGAA GTTCTTTTTA 3266
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286 TTGCTAAAAT ATTCTTCTC ACATATTCAT ATTCTCCAG 3355
287 GT GTT CCT GGC CAT CAT TTA AGG AAG AAT GAA GTG AAG TGT 3396
288 AGG ATG ATT TAT TTC TTC CAC GAC CCT AAT TTC CTG GTG TCT 3438
289 ATA CCA GTG AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT GAA 3480
290 AAT GCT GAT GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAA 3522
291 GAG GAG GAG GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC 3564
292 TTC TCA CCT TAG 3576
293 GCATGCAGGT ACTGGCTTCA CTAACCAACC ATTCCTAACA TATGCCTGTA 3626
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295 TCTTTTTACA TTAATAAGTA TTAATTAAT CCAGTATACA GTTTTAAGAA 3726
296 CCCTAAGTTA AACAGAAGTC AATGATGTCT AGATGCCCTGT TCTTTAGATT 3776
297 GCTGTGAGAC TACTTACTAC AGATGAGAAG TTGTTAGACT CGGGAGTAGA 3826
298 GACCAGTAAA AGATCATGCA GTGAAATGTG GCCATGGAAA TCGCATATTG 3876
299 TTCTTATAGT ACCTTTGAGA CAGCTGATAA CAGCTGACAA AAATAAGTGT 3926
300 TTCAAGAAAAG ATCACACGCC ATGGTTCACA TGCAAATTAT TATTTTGTCG 3976
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302 CTTAAAATTT CCTTCATCTT TAATTTTCCT TAACTTTAGT TTTTTCCTACT 4076
303 TAGAATTCAA TTCAAATCTT TAATTCAATC TTAATTTTAA GATTTCTTAA 4126
304 AATGTTTTTT AAAAAAATG CAAATCTCAT TTTTAAGAGA TGAAAGCAGA 4176
305 GTAAGTGGGG GGCTTAGGGA ATCTGTAGGG TTGCGGTATA GCAATAGGGA 4226
306 GTTCTGGTCT CTGAGAAGCA GTCAGAGAGA ATGGAAAACC AGGCCCTTGC 4276
307 CAGTAGGTTA GTGAGGTTGA TATGATCAGA TTATGGACAC TCTCCAAATC 4326
308 ATAAATACTC TAACAGCTAA GGATCTCTGA GGGAAACACA ACAGGGAAT 4376
309 ATTTTAGTTT CTCCTTGAGA AACAAATGACA AGACATAAAA TTGGCAAGAA 4426
310 AGTCAGGAGT GTATTCTAAT AAGTGTGCT TATCTCTTAT TTTCTTCTAC 4476
311 AGTTGCAAG CCCAGAAGAA AGAAATGGAC AGCGGAAGAA GTGGTTGTTT 4526
312 TTTTTTCCCC TTCAATTAAT TTCTAGTTTT TAGTAATCCA GAAAATTGA 4576
313 TTTTGTCTA AAGTTCATTA TGCAAAGATG TCACCAACAG ACTTCTGACT 4626
314 GCATGGTGAA CTTTCATATG ATACATAGGA TTACACTTGT ACCTGTTAAA 4676
315 AATAAAAGTT TGACTTGCAAT AC 4698
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318 (2) INFORMATION FOR SEQUENCE ID NO: 6:

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319 (i) SEQUENCE CHARACTERISTICS:
320 (A) LENGTH: 7 amino acids
321 (B) TYPE: amino acid
322 (C) STRANDEDNESS: singular
323 (D) TOPOLOGY: linear
324 (ii) MOLECULE TYPE: protein
325 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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327
328
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330 Leu Pro Tyr Leu Gly Trp Leu
331 5
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339 (2) INFORMATION FOR SEQUENCE ID NO: 7:
340 (i) SEQUENCE CHARACTERISTICS:
341 (A) LENGTH: 2419 base pairs
342 (B) TYPE: nucleic acid
343 (C) STRANDEDNESS: singular
344 (D) TOPOLOGY: linear
345 (ii) MOLECULE TYPE: genomic DNA
346 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
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351	GGATCCAGGC	CCTGCCAGGA	AAAATATAAG	GGCCCTGCGT	GAGAACAGAG	50
352	GGGGTCATCC	ACTGCATGAG	AGTGGGGATG	TCACAGAGTC	CAGCCCACCC	100
353	TCCTGGTAGC	ACTGAGAAGC	CAGGGCTGTG	CTTGCGGTCT	GCACCCTGAG	150
354	GGCCCGTGGA	TTCCTCTTCC	TGGAGCTCCA	GGAACCAGGC	AGTGAGGCCT	200
355	TGGTCTGAGA	CAGTATCCTC	AGGTCACAGA	GCAGAGGATG	CACAGGGTGT	250
356	GCCAGCAGTG	AATGTTTGCC	CTGAATGCAC	ACCAAGGGCC	CCACCTGCCA	300
357	CAGGACACAT	AGGACTCCAC	AGAGTCTGGC	CTCACCTCCC	TACTGTCAGT	350
358	CCTGTAGAAT	CGACCTCTGC	TGGCCGGCTG	TACCCTGAGT	ACCCTCTCAC	400
359	TTCCTCCTTC	AGGTTTTTCAG	GGGACAGGCC	AACCCAGAGG	ACAGGATTCC	450
360	CTGGAGGCCA	CAGAGGAGCA	CCAAGGAGAA	GATCTGTAAG	TAGGCCTTTG	500
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362	CTCTCCCCAG	GCCTGTGGGT	CTTCATTGCC	CAGCTCCTGC	CCACACTCCT	600
363	GCCTGCTGCC	CTGACGAGAG	TCATCATGTC	TCTTGAGCAG	AGGAGTCTGC	650
364	ACTGCAAGCC	TGAGGAAGCC	CTTGAGGCCC	AACAAGAGGC	CCTGGGCCTG	700
365	GTGTGTGTGC	AGGCTGCCAC	CTCCTCCTCC	TCTCCTCTGG	TCCTGGGCAC	750
366	CCTGGAGGAG	GTGCCCACATG	CTGGGTCAAC	AGATCCTCCC	CAGAGTCCTC	800
367	AGGGAGCCTC	CGCCTTTCCC	ACTACCATCA	ACTTCACTCG	ACAGAGGCAA	850
368	CCCAGTGAGG	GTTCCAGCAG	CCGTGAAGAG	GAGGGGCCAA	GCACCTCTTG	900
369	TATCCTGGAG	TCCTTGTTCC	GAGCAGTAAT	CACTAAGAAG	GTGGCTGATT	950
370	TGGTTGGTTT	TCTGCTCCTC	AAATATCGAG	CCAGGGAGCC	AGTCACAAAG	1000
371	GCAGAAATGC	TGGAGAGTGT	CATCAAAAAT	TACAAGCACT	GTTTTCCTGA	1050

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372 GATCTTCGGC AAAGCCTCTG AGTCCTTGCA GCTGGTCTTT GGCATTGACG 1100
373 TGAAGGAAGC AGACCCCACC GGCCACTCCT ATGTCCTTGT CACCTGCCTA 1150
374 GGTCTCTCCT ATGATGGCCT GCTGGGTGAT AATCAGATCA TGCCCAAGAC 1200
375 AGGCTTCCTG ATAATTGTCC TGGTCATGAT TGCAATGGAG GCGGCCATG 1250
376 CTCCTGAGGA GGAAATCTGG GAGGAGCTGA GTGTGATGGA GGTGTATGAT 1300
377 GGGAGGGAGC ACAGTGCCTA TGGGGAGCCC AGGAAGCTGC TCACCCAAGA 1350
378 TTTGGTGACG GAAAAGTACC TGGAGTACGG CAGGTGCCGG ACAGTGATCC 1400
379 CGCACGCTAT GAGTTCCTGT GGGGTCCAAG GGCCCTCGCT GAAACCAGCT 1450
380 ATGTGAAAGT CCTTGAGTAT GTGATCAAGG TCAGTGCAAG AGTTCGCTTT 1500
381 TTCTTCCCAT CCCTGCGTGA AGCAGCTTTG AGAGAGGAGG AAGAGGGAGT 1550
382 CTGAGCATGA GTTGCAGCCA AGGCCAGTGG GAGGGGGACT GGGCCAGTGC 1600
383 ACCTTCCAGG GCCGCGTCCA GCAGCTTCCC CTGCCTCGTG TGACATGAGG 1650
384 CCCATTCTTC ACTCTGAAGA GAGCGGTCAG TGTTCCTCAGT AGTAGGTTTC 1700
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386 TCAAATGTTT TTTTAAAGG GATGGTTGAA TGAACCTCAG CATCCAAGTT 1800
387 TATGAATGAC AGCAGTCACA CAGTTCGTG TATATAGTTT AAGGGTAAGA 1850
388 GTCTTGTTG TTATTCAGAT TGGGAAATCC ATTCTATTTT GTGAATTGGG 1900
389 ATAATAACAG CAGTGAATA AGTACTTAGA AATGTGAAA ATGAGCAGTA 1950
390 AAATAGATGA GATAAAGAAC TAAAGAAATT AAGAGATAGT CAATCTTGC 2000
391 CTTATACCTC AGTCTATTCT GTAAAATTTT TAAAGATATA TGCATACCTG 2050
392 GATTTCCCTG GCTTCTTTGA GAATGTAAGA GAAATTAAAT CTGAATAAAG 2100
393 AATTCTTCCT GTTCACTGGC TCTTTTCTTC TCCATGCACT GAGCATCTGC 2150
394 TTTTGGGAAG GCCCTGGGTT AGTAGTGGAG ATGCTAAGGT AAGCCAGACT 2200
395 CATACCCACC CATAGGGTCG TAGAGTCTAG GAGCTGCAGT CACGTAATCG 2250
396 AGGTGGCAAG ATGTCCTCTA AAGATGTAGG GAAAAGTGAG AGAGGGGTGA 2300
397 GGGTGTGGGG CTCCGGGTGA GAGTGGTGGG GTGTCAATGC CCTGAGCTGG 2350
398 GGCATTTTGG GCTTTGGGAA ACTGCAGTTC CTTCTGGGGG AGCTGATTGT 2400
399 AATGATCTTG GGTGGATCC 2419
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(2) INFORMATION FOR SEQUENCE ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5688 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: singular

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

(A) NAME/KEY: MAGE-1 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

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414 CCCGGGGCAC CACTGGCATC CCTCCCCCTA CCACCCCAA TCCCTCCCTT 50
415 TACGCCACCC ATCCAAACAT CTTACGCTC ACCCCCAGCC CAAGCCAGGC 100
416 AGAATCCGGT TCCACCCCTG CTCTCAACCC AGGGAAGCCC AGGTGCCAG 150
417 ATGTGACGCC ACTGACTTGA GCATTAGTGG TTAGAGAGAA GCGAGGTTTT 200
418 CGGTCTGAGG GCGGGCTTGA GATCGGTGGA GGGGAAGCGG CCCAGCTCTG 250
419 TAAGGAGGCA AGGTGACATG CTGAGGGAGG ACTGAGGACC CACTTACCCC 300
420 AGATAGAGGA CCCCCAATAA TCCCTTCATG CCAGTCCCTG ACCATCTGGT 350
421 GGTGGACTTC TCAGGCTGGG CCACCCCCAG CCCCCTTGCT GCTTAAACCA 400
422 CTGGGGACTC GAAGTCAGAG CTCCGTGTGA TCAGGGAAGG GCTGCTTAGG 450
423 AGAGGGCAGC GTCCAGGCTC TGCCAGACAT CATGCTCAGG ATTCTCAAGG 500
424 AGGGCTGAGG GTCCCTAAGA CCCCCTCCC GTGACCCAAC CCCCCTCCA 550
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5674 are listed

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425	ATGCTCACTC	CCGTGACCCA	ACCCCTCTT	CATTGTCATT	CCAACCCCA	600
426	CCCCACATCC	CCCACCCCAT	CCCTCAACCC	TGATGCCCAT	CCGCCCAGCC	650
427	ATTCCACCCCT	CACCCCCACC	CCCACCCCA	CGCCCACTCC	CACCCCCACC	700
428	CAGGCAGGAT	CCGGTTCCTG	CCAGGAAACA	TCCGGGTGCC	CGGATGTGAC	750
429	GCCACTGACT	TGCGCATTGT	GGGGCAGAGA	GAAGCGAGGT	TTCCATTCTG	800
430	AGGGACGGCG	TAGAGTTCGG	CCGAAGGAAC	CTGACCCAGG	CTCTGTGAGG	850
431	AGGCAAGGTG	AGAGGCTGAG	GGAGGACTGA	GGACCCCGCC	ACTCCAAATA	900
432	GAGAGCCCCA	AATATTCCAG	CCCCGCCCTT	GCTGCCAGCC	CTGGCCCACC	950
433	CGCGGGAAGA	CGTCTCAGCC	TGGGCTGCCC	CCAGACCCCT	GCTCCAAAAG	1000
434	CCTTGAGAGA	CACCAGGTTC	TTCTCCCCAA	GCTCTGGAAT	CAGAGGTTGC	1050
435	TGTGACCAGG	GCAGGACTGG	TTAGGAGAGG	GCAGGGCACA	GGCTCTGCCA	1100
436	GGCATCAAGA	TCAGCACCCA	AGAGGGAGGG	CTGTGGGCCC	CCAAGACTGC	1150
437	ACTCCAATCC	CCACTCCCAC	CCCATTGCGA	TTCCCATTCC	CCACCCAACC	1200
438	CCCATCTCCT	CAGCTACACC	TCCACCCCA	TCCCTACTCC	TACTCCGTCA	1250
439	CCTGACCACC	ACCCCTCAGC	CCCAGCACC	GCCCCAACCC	TTCTGCCACC	1300
440	TCACCCTCAC	TGCCCCAAC	CCCACCTCA	TCTCTCTCAT	GTGCCCCACT	1350
441	CCCATCGCCT	CCCCCATTC	GGCAGAATCC	GGTTTGCCCC	TGCTCTCAAC	1400
442	CCAGGGAAGC	CCTGCTAGGC	CCGATGTGAA	ACCATGACT	TGAACCTCAC	1450
443	AGATCTGAGA	GAGGCCAGGT	TCATTTAATG	GTTCTGAGGG	GCGGCTTGAG	1500
444	ATCCACTGAG	GGGAGTGGTT	TTAGGCTCTG	TGAGGAGGCA	AGGTGAGATG	1550
445	CTGAGGGAGG	ACTGAGGAGG	CACACACCCC	AGGTAGATGG	CCCCAAAATG	1600
446	ATCCAGTACC	ACCCCTGCTG	CCAGCCCTGG	ACCACCCGGC	CAGGACAGAT	1650
447	GTCTCAGCTG	GACCACCCCC	CGTCCCCTCC	CACTGCCACT	TAACCCACAG	1700
448	GGCAATCTGT	AGTCATAGCT	TATGTGACCG	GGGCAGGGTT	GGTCAGGAGA	1750
449	GGCAGGGCCC	AGGCATCAAG	GTCCAGCATC	CGCCCGGCAT	TAGGGTCAGG	1800
450	ACCCTGGGAG	GGAACTGAGG	GTTCCCCACC	CACACCTGTC	TCCTCATCTC	1850
451	CACCGCCACC	CCACTCACAT	TCCCATACCT	ACCCCTTACC	CCCAACCTCA	1900
452	TCTTGTGAGA	ATCCCTGCTG	TCAACCCACG	GAAGCCACGG	GAATGGCGGC	1950
453	CAGGCACTCG	GATCTTGACG	TCCCCATCCA	GGGTCTGATG	GAGGGAAGGG	2000
454	GCTTGAACAG	GGCCTCAGGG	GAGCAGAGGG	AGGGCCCTAC	TGCGAGATGA	2050
455	GGGAGGCCTC	AGAGGACCCA	GCACCCTAGG	ACACCGCACC	CCTGTCTGAG	2100
456	ACTGAGGCTG	CCACTTCTGG	CCTCAAGAAT	CAGAACGATG	GGGACTCAGA	2150
457	TTGCATGGGG	GGGGACCCA	GGCCTGCAAG	GCTTACGCGG	AGGAAGAGGA	2200
458	GGGAGGACTC	AGGGGACCTT	GGAATCCAGA	TCAGTGTGGA	CCTCGGCCCT	2250
459	GAGAGGTCCA	GGGCACGGTG	GCCACATATG	GCCCATATTT	CCTGCATCTT	2300
460	TGAGGTGACA	GGACAGAGCT	GTGGTCTGAG	AAGTGGGGCC	TCAGGTCAAC	2350
461	AGAGGGAGGA	GTTCCAGGAT	CCATATGGCC	CAAGATGTGC	CCCCTTCATG	2400
462	AGGACTGGGG	ATATCCCCGG	CTCAGAAAGA	AGGGACTCCA	CACAGTCTGG	2450
463	CTGTCCCCTT	TTAGTAGCTC	TAGGGGGACC	AGATCAGGGA	TGGCGGTATG	2500
464	TTCCATTCTC	ACTTGTACCA	CAGGCAGGAA	GTTGGGGGGC	CCTCAGGGAG	2550
465	ATGGGGTCTT	GGGGTAAAGG	GGGGATGTCT	ACTCATGTCA	GGGAATTGGG	2600
466	GGTTGAGGAA	GCACAGGCGC	TGGCAGGAAT	AAAGATGAGT	GAGACAGACA	2650
467	AGGCTATTGG	AATCCACACC	CCAGAACCBA	AGGGGTGAGC	CCTGGACACC	2700
468	TCACCCAGGA	TGTGGCTTCT	TTTTCACCTC	TGTTTCCAGA	TCTGGGGCAG	2750
469	GTGAGGACCT	CATTCTCAGA	GGGTGACTCA	GGTCAACGTA	GGGACCCCA	2800
470	TCTGGTCTAA	AGACAGAGCG	GTCCCAGGAT	CTGCCATGCG	TTCGGGTGAG	2850
471	GAACATGAGG	GAGGACTGAG	GGTACCCAG	GACCAGAACA	CTGAGGGAGA	2900
472	CTGCACAGAA	ATCAGCCCTG	CCCCTGCTGT	CACCCAGAG	AGCATGGGCT	2950
473	GGGCCGTCTG	CCGAGGTCTT	TCCGTTATCC	TGGGATCATT	GATGTCAGGG	3000
474	ACGGGGAGGC	CTTGGTCTGA	GAAGGCTGCG	CTCAGGTCAG	TAGAGGGAGC	3050
475	GTCCCAGGCC	CTGCCAGGAG	TCAAGGTGAG	GACCAAGCGG	GCACCTCACC	3100
476	CAGGACACAT	TAATTCCAAT	GAATTTTGAT	ATCTCTTGCT	GCCCTTCCCC	3150
477	AAGGACCTAG	GCACGTGTGG	CCAGATGTTT	GTCCCTCTCT	GTCCTTCCAT	3200

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478	TCCTTATCAT	GGATGTGAAC	TCTTGATTTC	GATTTCTCAG	ACCAGCAAAA	3250
479	GGGAGGATC	CAGGCCCTGC	CAGGAAAAAT	ATAAGGGCCC	TGCGTGAGAA	3300
480	CAGAGGGGGT	CATCCACTGC	ATGAGAGTGG	GGATGTCACA	GAGTCCAGCC	3350
481	CACCCCTCCTG	GTAGCACTGA	GAAGCCAGGG	CTGTGCTTGC	GGTCTGCACC	3400
482	CTGAGGGCCC	GTGGATTCCCT	CTTCCTGGAG	CTCCAGGAAC	CAGGCAGTGA	3450
483	GGCCTTGGTC	TGAGACAGTA	TCCTCAGGTC	ACAGAGCAGA	GGATGCACAG	3500
484	GGTGTGCCAG	CAGTGAATGT	TTGCCCTGAA	TGCACACCAA	GGGCCCCACC	3550
485	TGCCACAGGA	CACATAGGAC	TCCACAGAGT	CTGGCCTCAC	CTCCCTACTG	3600
486	TCAGTCTGT	AGAATCGACC	TCTGCTGGCC	GGCTGTACCC	TGAGTACCCT	3650
487	CTCACTTCCT	CCTTCAGGTT	TTCAGGGGAC	AGGCCAACCC	AGAGGACAGG	3700
488	ATTCCCTGGA	GGCCACAGAG	GAGCACCAAG	GAGAAGATCT	GTAAGTAGGC	3750
489	CTTTGTTAGA	GTCTCCAAGG	TTCAGTTCTC	AGCTGAGGCC	TCTCACACAC	3800
490	TCCCTCTCTC	CCCAGGCCCTG	TGGGTCTTCA	TTGCCCAGCT	CCTGCCCACA	3850
491	CTCCTGCCTG	CTGCCCTGAC	GAGAGTCATC			3880
492	ATG TCT CTT	GAG CAG AGG	AGT CTG CAC	TGC AAG CCT	GAG GAA	3922
493	GCC CTT GAG	GCC CAA CAA	GAG GCC CTG	GGC CTG GTG	TGT GTG	3964
494	CAG GCT GCC	ACC TCC TCC	TCT CCT CTG	GTC CTG GGC	ACC	4006
495	CTG GAG GAG	GTG CCC ACT	GCT GGG TCA	ACA GAT CCT	CCC CAG	4048
496	AGT CCT CAG	GGG GCC TCC	GCC TTT CCC	ACT ACC ATC	AAC TTC	4090
497	ACT CGA CAG	AGG CAA CCC	AGT GAG GGT	TCC AGC AGC	CGT GAA	4132
498	GAG GAG GGG	CCA AGC ACC	TCT TGT ATC	CTG GAG TCC	TTG TTC	4174
499	CGA GCA GTA	ATC ACT AAG	AAG GTG GCT	GAT TTG GTT	GGT TTT	4216
500	CTG CTC CTC	AAA TAT CGA	GCC AGG GAG	CCA GTC ACA	AAG GCA	4258
501	GAA ATG CTG	GAG AGT GTC	ATC AAA AAT	TAC AAG CAC	TGT TTT	4300
502	CCT GAG ATC	TTC GGC AAA	GCC TCT GAG	TCC TTG CAG	CTG GTC	4342
503	TTT GGC ATT	GAC GTG AAG	GAA GCA GAC	CCC ACC GGC	CAC TCC	4384
504	TAT GTC CTT	GTC ACC TGC	CTA GGT CTC	TCC TAT GAT	GGC CTG	4426
505	CTG GGT GAT	AAT CAG ATC	ATG CCC AAG	ACA GGC TTC	CTG ATA	4468
506	ATT GTC CTG	GTC ATG ATT	GCA ATG GAG	GGC GGC CAT	GCT CCT	4510
507	GAG GAG GAA	ATC TGG GAG	GAG CTG AGT	GTG ATG GAG	GTG TAT	4552
508	GAT GGG AGG	GAG CAC AGT	GCC TAT GGG	GAG CCC AGG	AAG CTG	4594
509	CTC ACC CAA	GAT TTG GTG	CAG GAA AAG	TAC CTG GAG	TAC GGC	4636
510	AGG TGC CGG	ACA GTG ATC	CCG CAC GCT	ATG AGT TCC	TGT GGG	4678
511	GTC CAA GGG	CCC TCG CTG	AAA CCA GCT	ATG TGA		4711
512	AAGTCCTTGA	GTATGTGATC	AAGGTCAGTG	CAAGAGTTC		4750
513	GCTTTTTCTT	CCCATCCCTG	CGTGAAGCAG	CTTTGAGAGA	GGAGGAAGAG	4800
514	GGAGTCTGAG	CATGAGTTGC	AGCCAAGGCC	AGTGGGAGGG	GGACTGGGCC	4850
515	AGTGCACCTT	CCAGGGCCGC	GTCCAGCAGC	TTCCCCCTGCC	TCGTGTGACA	4900
516	TGAGGCCCCAT	TCTTCACTCT	GAAGAGAGCG	GTCAGTGTTT	TCAGTAGTAG	4950
517	GTTTCTGTTC	TATTGGGTGA	CTTGGAGATT	TATCTTTGTT	CTCTTTTGGA	5000
518	ATTGTTCAAA	TGTTTTTTTT	TAAGGGATGG	TTGAATGAAC	TTCAGCATCC	5050
519	AAGTTTATGA	ATGACAGCAG	TCACACAGTT	CTGTGTATAT	AGTTTAAGGG	5100
520	TAAGAGTCTT	GTGTTTTATT	CAGATTGGGA	AATCCATTCT	ATTTTGTGAA	5150
521	TTGGGATAAT	AACAGCAGTG	GAATAAGTAC	TTAGAAATGT	GAAAAATGAG	5200
522	CAGTAAAATA	GATGAGATAA	AGAACTAAAG	AAATTAAGAG	ATAGTCAATT	5250
523	CTTGCCCTTAT	ACCTCAGTCT	ATTCTGTAAA	ATTTTAAAG	ATATATGCAT	5300
524	ACCTGGATTT	CCTTGGCTTC	TTTGAGAATG	TAAGAGAAAT	TAAATCTGAA	5350
525	TAAAGAATTC	TTCCTGTTCA	CTGGCTCTTT	TGAGATGCT	GCAGTAAGCC	5400
526	TCTGCTTTTT	GGGAGGCCCT	GGGTAGTAG	TGGAGATGCT	AAGGTAAGCC	5450
527	AGACTCATAC	CCACCCATAG	GGTCGTAGAG	TCTAGGAGCT	GCAGTCACGT	5500
528	AATCGAGGTG	GCAAGATGTC	CTCTAAAGAT	GTAGGGAAAA	GTGAGAGAGG	5550
529	GGTGAGGGTG	TGGGGCTCCG	GGTGAGAGTG	GTGGAGTGTC	AATGCCCTGA	5600
530	GCTGGGGCAT	TTTGGGCTTT	GGGAACTGC	AGTTCCTTCT	GGGGGAGCTG	5650

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531 ATTGTAATGA TCTTGGGTGG ATCC

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536 (2) INFORMATION FOR SEQUENCE ID NO: 9:

537 (i) SEQUENCE CHARACTERISTICS:

538 (A) LENGTH: 4157 base pairs

539 (B) TYPE: nucleic acid

540 (C) STRANDEDNESS: singular

541 (D) TOPOLOGY: linear

542 (ii) MOLECULE TYPE: genomic DNA

543 (ix) FEATURE:

544 (A) NAME/KEY: MAGE-2 gene

545 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

546
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549	CCCATCCAGA	TCCCCATCCG	GGCAGAATCC	GGTTCCACCC	TTGCCGTGAA	50
550	CCCAGGGGAA	TCACGGGCCC	GGATGTGACG	CCACTGACTT	GCACATTGGA	100
551	GGTCAGAGGA	CAGCGAGATT	CTCGCCCTGA	GCAACGGCCT	GACGTCGGCG	150
552	GAGGGAAGCA	GGCGCAGGCT	CCGTGAGGAG	GCAAGGTAAG	ACGCCGAGGG	200
553	AGGACTGAGG	CGGGCCTCAC	CCCAGACAGA	GGGCCCCCAA	TTAATCCAGC	250
554	GCTGCCTCTG	CTGCCGGGCC	TGGACCACCC	TGCAGGGGAA	GACTTCTCAG	300
555	GCTCAGTCGC	CACCACCTCA	CCCCGCCACC	CCCCGCCGCT	TTAACCGCAG	350
556	GGAACTCTGG	CGTAAGAGCT	TTGTGTGACC	AGGGCAGGGC	TGGTTAGAAG	400
557	TGCTCAGGGC	CCAGACTCAG	CCAGGAATCA	AGGTCAGGAC	CCCAAGAGGG	450
558	GACTGAGGGC	AACCCACCCC	CTACCCTCAC	TACCAATCCC	ATCCCCCAAC	500
559	ACCAACCCCA	CCCCCATCCC	TCAAACACCA	ACCCACCCC	CAAACCCCAT	550
560	TCCCATCTCC	TCCCCACCA	CCATCCTGGC	AGAATCCGGC	TTTGCCCCCTG	600
561	CAATCAACCC	ACGGAAGCTC	CGGGAATGGC	GGCCAAGCAC	GCGGATCCTG	650
562	ACGTTACAT	GTACGGCTAA	GGGAGGGAAG	GGGTTGGGTC	TCGTGAGTAT	700
563	GGCCTTTGGG	ATGCAGAGGA	AGGGCCCAGG	CCTCCTGGAA	GACAGTGGAG	750
564	TCCTTAGGGG	ATCCAGCATG	CCAGGACAGG	GGGCCCACTG	TACCCCTGTC	800
565	TCAAACCTGAG	CCACCTTTTC	ATTCAGCCGA	GGGAATCCTA	GGGATGCAGA	850
566	CCCACTTCAG	GGGGTTGGGG	CCCAGCCTGC	GAGGAGTCAA	GGGGAGGAAG	900
567	AAGAGGGAGG	ACTGAGGGGA	CCTTGGAGTC	CAGATCAGTG	GCAACCTTGG	950
568	GCTGGGGGAT	CCTGGGCACA	GTGGCCGAAT	GTGCCCCGTG	CTCATTCGAC	1000
569	CTTCAGGGTG	ACAGAGAGTT	GAGGGCTGTG	GTCTGAGGGC	TGGGACTTCA	1050
570	GGTCAGCAGA	GGGAGGAATC	CCAGGATCTG	CCGGACCCAA	GGTGTGCCCC	1100
571	CTTCATGAGG	ACTCCCCATA	CCCCCGGCCC	AGAAAGAAGG	GATGCCACAG	1150
572	AGTCTGGAAG	TAAATTGTTC	TTAGCTCTGG	GGGAACCTGA	TCAGGGATGG	1200
573	CCCTAAGTGA	CAATCTCATT	TGTACCACAG	GCAGGAGGTT	GGGGAACCTT	1250
574	CAGGGAGATA	AGGTGTTGGT	GTAAAGAGGA	GCTGTCTGCT	CATTTAGGG	1300
575	GGTTCCCCCT	TGAGAAAGGG	CAGTCCCTGG	CAGGAGTAA	GATGAGTAAC	1350
576	CCACAGGAGG	CCATCATAAC	GTTCAACCCTA	GAACCAAAGG	GGTCAGCCCT	1400
577	GGACAACGCA	CGTGGGGTAA	CAGGATGTGG	CCCCCTCTCA	CTTGTCTTTC	1450
578	GAGATCTCAG	GGAGTTGATG	ACCTTGTTTT	CAGAAGGTGA	CTCAGTCAAC	1500
579	ACAGGGGCCC	CTCTGGTCTGA	CAGATGCAGT	GGTTCCTAGGA	TCTGCCAAGC	1550
580	ATCCAGGTGG	AGAGCCTGAG	GTAGGATTGA	GGGTACCCCT	GGGCCAGAAT	1600
581	GCAGCAAGGG	GGCCCCATAG	AAATCTGCCC	TGCCCCCTGCG	GTTACTTCAG	1650
582	AGACCCTGGG	CAGGGCTGTC	AGCTGAAGTC	CCTCCATTAT	CTGGGATCTT	1700
583	TGATGTCAGG	GAAGGGGAGG	CCTTGGTCTG	AAGGGGCTGG	AGTCAGGTCA	1750

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584	GTAGAGGGAG	GGTCTCAGGC	CCTGCCAGGA	GTGGACGTGA	GGACCAAGCG	1800
585	GACTCGTCAC	CCAGGACACC	TGGACTCCAA	TGAATTTGAC	ATCTCTCGTT	1850
586	GTCTTTCGCG	GAGGACCTGG	TCACGTATGG	CCAGATGTGG	GTCCCCCTCTA	1900
587	TCTCCTTCTG	TACCATATCA	GGGATGTGAG	TTCTTGACAT	GAGAGATTCT	1950
588	CAAGCCAGCA	AAAGGGTGGG	ATTAGGCCCT	ACAAGGAGAA	AGGTGAGGGC	2000
589	CCTGAGTGAG	CACAGAGGGG	ACCCTCCACC	CAAGTAGAGT	GGGGACCTCA	2050
590	CGGAGTCTGG	CCAACCCTGC	TGAGACTTCT	GGGAATCCGT	GGCTGTGCTT	2100
591	GCAGTCTGCA	CACTGAAGGC	CCGTGCATTC	CTCTCCCAGG	AATCAGGAGC	2150
592	TCCAGGAACC	AGGCAGTGAG	GCCTTGGTCT	GAGTCAGTGC	CTCAGGTCAC	2200
593	AGAGCAGAGG	GGACGCAGAC	AGTGCCAACA	CTGAAGGTTT	GCCTGGAATG	2250
594	CACACCAAGG	GCCCCACCCG	CCCAGAACAA	ATGGGACTCC	AGAGGGCCTG	2300
595	GCCTCACCCCT	CCCTATTCTC	AGTCCTGCAG	CCTGAGCATG	TGCTGGCCGG	2350
596	CTGTACCCTG	AGGTGCCCCC	CCACTTCCTC	CTTCAGGTTT	TGAGGGGGAC	2400
597	AGGCTGACAA	GTAGGACCCG	AGGCACTGGA	GGAGCATTTA	AGGAGAAGAT	2450
598	CTGTAAGTAA	GCCTTTGTCA	GAGCCTCCAA	GGTTCAGTTC	AGTTCTCACC	2500
599	TAAGGCCTCA	CACACGCTCC	TTCTCTCCCC	AGGCCTGTGG	GTCTTCATTG	2550
600	CCAGCTCCT	GCCCGCAGTC	CTGCCCTGCTG	CCCTGACCAG	AGTCATC	2597
601	ATG CCT CTT	GAG CAG AGG	AGT CAG CAC	TGC AAG CCT	GAA GAA	2639
602	GGC CTT GAG	GCC CGA GGA	GAG GCC CTG	GGC CTG GTG	GGT GCG	2681
603	CAG GCT CCT	GCT ACT GAG	GAG CAG CAG	ACC GCT TCT	TCC TCT	2723
604	TCT ACT CTA	GTG GAA GTT	ACC CTG GGG	GAG GTG CCT	GCT GCC	2765
605	GAC TCA CCG	AGT CCT CCC	CAC AGT CCT	CAG GGA GCC	TCC AGC	2807
606	TTC TCG ACT	ACC ATC AAC	TAC ACT CTT	TGG AGA CAA	TCC GAT	2849
607	GAG GGC TCC	AGC AAC CAA	GAA GAG GAG	GGG CCA AGA	ATG TTT	2891
608	CCC GAC CTG	GAG TCC GAG	TTC CAA GCA	GCA ATC AGT	AGG AAG	2933
609	ATG GTT GAG	TTG GTT CAT	TTT CTG CTC	CTC AAG TAT	CGA GCC	2975
610	AGG GAG CCG	GTC ACA AAG	GCA GAA ATG	CTG GAG AGT	GTC CTC	3017
611	AGA AAT TGC	CAG GAC TTC	TTT CCC GTG	ATC TTC AGC	AAA GCC	3059
612	TCC GAG TAC	TTG CAG CTG	GTC TTT GGC	ATC GAG GTG	GTG GAA	3101
613	GTG GTC CCC	ATC AGC CAC	TTG TAC ATC	CTT GTC ACC	TGC CTG	3143
614	GGC CTC TCC	TAC GAT GGC	CTG CTG GGC	GAC AAT CAG	GTC ATG	3185
615	CCC AAG ACA	GGC CTC CTG	ATA ATC GTC	CTG GCC ATA	ATC GCA	3227
616	ATA GAG GGC	GAC TGT GCG	CCT GAG GAG	AAA ATC TGG	GAG GAG	3269
617	CTG AGT ATG	TTG GAG GTG	TTT GAG GGG	AGG GAG GAC	AGT GTC	3311
618	TTC GCA CAT	CCC AGG AAG	CTG CTC ATG	CAA GAT CTG	GTG CAG	3353
619	GAA AAC TAC	CTG GAG TAC	CGG CAG GTG	CCC GGC AGT	GAT CCT	3395
620	GCA TGC TAC	GAG TTC CTG	TGG GGT CCA	AGG GCC CTC	ATT GAA	3437
621	ACC AGC TAT	GTG AAA GTC	CTG CAC CAT	ACA CTA AAG	ATC GGT	3479
622	GGA GAA CCT	CAC ATT TCC	TAC CCA CCC	CTG CAT GAA	CGG GCT	3521
623	TTG AGA GAG	GGA GAA GAG	TGA			3542
624	GTCTCAGCAC	ATGTTGCAGC	CAGGGCCAGT	GGGAGGGGGT	CTGGGCCAGT	3592
625	GCACCTTCCA	GGGCCCCATC	CATTAGCTTC	CAGTGCCTCG	TGTGATATGA	3642
626	GGCCCATTC	TGCCTCTTTG	AAGAGAGCAG	TCAGCATCT	TAGCAGTGAG	3692
627	TTTCTGTTCT	GTTGGATGAC	TTTGAGATTT	ATCTTTCTTT	CCTGTTGGAA	3742
628	TTGTTCAAAAT	GTTCTTTTA	ACAAATGGTT	GGATGAACCT	CAGCATCCAA	3792
629	TTTATGAAT	GACAGTAGTC	ACACATAGTG	CTGTTTATAT	AGTTTAGGGG	3842
630	TAAGAGTCCT	GTTTTTTATT	CAGATTGGGA	AATCCATTCC	ATTTTGTGAG	3892
631	TTGTACATA	ATAACAGCAG	TGGAATATGT	ATTTCCTAT	ATTGTGAACG	3942
632	AATTAGCAGT	AAAATACATG	ATACAAGGAA	CTCAAAAGAT	AGTTAATTCT	3992
633	TGCCTTATAC	CTCAGTCTAT	TATGTAAAAT	TAAAAATATG	TGTATGTTTT	4042
634	TGCTTCTTTG	AGAATGCAAA	AGAAATTAAA	TCTGAATAAA	TTCTTCCTGT	4092
635	TCAGTGGCTC	ATTTCTTTAC	CATTCACCTCA	GCATCTGCTC	TGTGGAAGGC	4142
636	CCTGGTAGTA	GTGGG				4157

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(2) INFORMATION FOR SEQUENCE ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 662 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: singular
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: MAGE-21 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GGATCCCCAT	GGATCCAGGA	AGAATCCAGT	TCCACCCCTG	CTGTGAACCC	50
AGGGAAGTCA	CGGGGCCGGA	TGTGACGCCA	CTGACTTGCG	CGTTGGAGGT	100
CAGAGAACAG	CGAGATTCTC	GCCCTGAGCA	ACGGCCTGAC	GTCGGCGGAG	150
GGAAGCAGGC	GCAGGCTCCG	TGAGGAGGCA	AGGTAAGATG	CCGAGGGAGG	200
ACTGAGGCGG	GCCTCACCCC	AGACAGAGGG	CCCCCAATAA	TCCAGCGCTG	250
CCTCTGCTGC	CAGGCCTGGA	CCACCCTGCA	GGGGAAGACT	TCTCAGGCTC	300
AGTCGCCACC	ACCTCACCCC	GCCACCCCCC	GCCGCTTTAA	CCGCAGGGAA	350
CTCTGGTGTA	AGAGCTTTGT	GTGACCAGGG	CAGGGCTGGT	TAGAAGTGCT	400
CAGGGCCCA	ACTCAGCCAG	GAATCAAGGT	CAGGACCCCA	AGAGGGGACT	450
GAGGGTAACC	CCCCCGCACC	CCCACCACCA	TTCCCATCCC	CCAACACCAA	500
CCCCACCCCC	ATCCCCCAAC	ACCAAACCCA	CCACCATCGC	TCAAACATCA	550
ACGGCACCCC	CAAACCCCGA	TTCCCATCCC	CACCCATCCT	GGCAGAATCG	600
GAGCTTTGCC	CCTGCAATCA	ACCCACGGAA	GCTCCGGGAA	TGGCGGCCAA	650
GCACGCGGAT	CC				662

(2) INFORMATION FOR SEQUENCE ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1640 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: singular
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(ix) FEATURE:

- (A) NAME/KEY: cDNA MAGE-3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

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690
691 GCCGCGAGGG AAGCCGGCCC AGGCTCGGTG AGGAGGCAAG GTTCTGAGGG 50
692 GACAGGCTGA CCTGGAGGAC CAGAGGCCCC CGGAGGAGCA CTGAAGGAGA 100
693 AGATCTGCCA GTGGGTCTCC ATTGCCCAGC TCCTGCCCAC ACTCCCGCCT 150
694 GTTGCCCTGA CCAGATCAT C 171
695 ATG CCT CTT GAG CAG AGG AGT CAG CAC TGC AAG CCT GAA GAA 213
696 GGC CTT GAG GCC CGA GGA GAG GCC CTG GGC CTG GTG GGT GCG 255
697 CAG GCT CCT GCT ACT GAG GAG CAG GAG GCT GCC TCC TCC TCT 297
698 TCT ACT CTA GTT GAA GTC ACC CTG GGG GAG GTG CCT GCT GCC 339
699 GAG TCA CCA GAT CCT CCC CAG AGT CCT CAG GGA GCC TCC AGC 381
700 CTC CCC ACT ACC ATG AAC TAC CCT CTC TGG AGC CAA TCC TAT 423
701 GAG GAC TCC AGC AAC CAA GAA GAG GAG GGG CCA AGC ACC TTC 465
702 CCT GAC CTG GAG TCC GAG TTC CAA GCA GCA CTC AGT AGG AAG 507
703 GTG GCC GAG TTG GTT CAT TTT CTG CTC CTC AAG TAT CGA GCC 549
704 AGG GAG CCG GTC ACA AAG GCA GAA ATG CTG GGG AGT GTC GTC 591
705 GGA AAT TGG CAG TAT TTC TTT CCT GTG ATC TTC AGC AAA GCT 633
706 TCC AGT TCC TTG CAG CTG GTC TTT GGC ATC GAG CTG ATG GAA 675
707 GTG GAC CCC ATC GGC CAC TTG TAC ATC TTT GCC ACC TGC CTG 717
708 GGC CTC TCC TAC GAT GGC CTG CTG GGT GAC AAT CAG ATC ATG 759
709 CCC AAG GCA GGC CTC CTG ATA ATC GTC CTG GCC ATA ATC GCA 801
710 AGA GAG GGC GAC TGT GCC CCT GAG GAG AAA ATC TGG GAG GAG 843
711 CTG AGT GTG TTA GAG GTG TTT GAG GGG AGG GAA GAC AGT ATG 885
712 TTG GGG GAT CCC AAG AAG CTG CTC ACC CAA CAT TTC GTG CAG 927
713 GAA AAC TAC CTG GAG TAC CGG CAG GTC CCC GGC AGT GAT CCT 969
714 GCA TGT TAT GAA TTC CTG TGG GGT CCA AGG GCC CTC GTT GAA 1011
715 ACC AGC TAT GTG AAA GTC CTG CAC CAT ATG GTA AAG ATC AGT 1053
716 GGA GGA CCT CAC ATT TCC TAC CCA CCC CTG CAT GAG TGG GTT 1095
717 TTG AGA GAG GGG GAA GAG TGA 1116
718 GTCTGAGCAC GAGTTGCAGC CAGGGCCAGT GGGAGGGGGT CTGGGCCAGT 1166
719 GCACCTTCCG GGGCCGCATC CCTTAGTTTC CACTGCCTCC TGTGACGTGA 1216
720 GGCCCATTTCT TCACTCTTTG AAGCGAGCAG TCAGCATTCT TAGTAGTGGG 1266
721 TTTCTGTTCT GTTGATGAC TTTGAGATTA TTCTTTGTTT CCTGTTGGAG 1316
722 TTGTTCAAAT GTTCCTTTA ACGGATGGTT GAATGAGCGT CAGCATCCAG 1366
723 GTTTATGAAT GACAGTAGTC ACACATAGTG CTGTTTATAT AGTTTAGGAG 1416
724 TAAGAGTCTT GttTTTTACT CAAATTgGGA AATCCATTCC ATTTTGTGAA 1466
725 TTGTGACATA ATAATAGCAG TGGTAAAAGT ATTTGCTTAA AATTGTGAGC 1516
726 GAATTAGCAA TAACATACAT GAGATAACTC AAGAAATCAA AAGATAGTTG 1566
727 ATTCTTGCCCT TGTACCTCAA TCTATTCTGT AAAATTAAAC AAATATGCAA 1616
728 ACCAGGATTT CCTTGACTTC TTG 1640
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733 (2) INFORMATION FOR SEQUENCE ID NO: 12:

734 (i) SEQUENCE CHARACTERISTICS:

735 (A) LENGTH: 943 base pairs

736 (B) TYPE: nucleic acid

737 (C) STRANDEDNESS: singular

738 (D) TOPOLOGY: linear

739 (ii) MOLECULE TYPE: genomic DNA

740 (ix) FEATURE:

741 (A) NAME/KEY: MAGE-31 gene

742 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

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746 GGATCCTCCA CCCAGTAGA GTGGGGACCT CACAGAGTCT GGCCAACCCT 50
747 CCTGACAGTT CTGGGAATCC GTGGCTGCGT TTGCTGTCTG CACATTGGGG 100
748 GCCCGTGGAT TCCTCTCCCA GGAATCAGGA GCTCCAGGAA CAAGGCAGTG 150
749 AGGACTTGGT CTGAGGCAGT GTCCTCAGGT CACAGAGTAG AGGGGgCTCA 200
750 GATAGTGCCA ACGGTGAAGG TTTGCCTTGG ATTCAAACCA AGGGCCCCAC 250
751 CTGCCCCAGA ACACATGGAC TCCAGAGCGC CTGGCCTCAC CCTCAATACT 300
752 TTCAGTCCTG CAGCCTCAGC ATGCGCTGGC CGGATGTACC CTGAGGTGCC 350
753 CTCTCACTTC CTCCTTCAGG TTCTGAGGGG ACAGGCTGAC CTGGAGGACC 400
754 AGAGGCCCCC GGAGGAGCAC TGAAGGAGAA GATCTGTAAG TAAGCCTTTG 450
755 TTAGAGCCTC CAAGGTTCCTC TTCAGTACTC AGCTGAGGTC TCTCACATGC 500
756 TCCCTCTCTC CCCAGGCCAG TGGGTCTCCA TTGCCCAGCT CCTGCCCACA 550
757 CTCCCGCCTG TTGCCCTGAC CAGAGTCATC 580
758 ATG CCT CTT GAG CAG AGG AGT CAG CAC TGC AAG CCT GAA GAA 622
759 GGC CTT GAG GCC CGA GGA GAg GCC CTG GGC CTG GTG GGT GCG 664
760 CAG GCT CCT GCT ACT GAG GAG CAG GAG GCT GCC TCC TCC TCT 706
761 TCT AGT GTA GTT GAA GTC ACC CTG GGG GAG GTG CCT GCT GCC 748
762 GAG TCA CCA GAT CCT CCC CAG AGT CCT CAG GGA GCC TCC AGC 790
763 CTC CCC ACT ACC ATG AAC TAC CCT CTC TGG AGC CAA TCC TAT 832
764 GAG GAC TCC AGC AAC CAA GAA GAG GAG GGG CCA AGC ACC TTC 874
765 CCT GAC CTG GAG TCT GAG TTC CAA GCA GCA CTC AGT AGG AAG 916
766 GTG GCC AAG TTG GTT CAT TTT CTG CTC 943

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771 (2) INFORMATION FOR SEQUENCE ID NO: 13:

772 (i) SEQUENCE CHARACTERISTICS:

773 (A) LENGTH: 1067 base pairs

774 (B) TYPE: nucleic acid

775 (C) STRANDEDNESS: singular

776 (D) TOPOLOGY: linear

777 (ii) MOLECULE TYPE: cDNA to mRNA

778 (ix) FEATURE:

779 (A) NAME/KEY: cDNA MAGE-4

780 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

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784 GGG CCA AGC ACC TCG CCT GAC GCA GAG TCC TTG TTC CGA 39
785 GAA GCA CTC AGT AAC AAG GTG GAT GAG TTG GCT CAT TTT CTG 81
786 CTC CGC AAG TAT CGA GCC AAG GAG CTG GTC ACA AAG GCA GAA 123
787 ATG CTG GAG AGA GTC ATC AAA AAT TAC AAG CGC TGC TTT CCT 165
788 GTG ATC TTC GGC AAA GCC TCC GAG TCC CTG AAG ATG ATC TTT 207
789 GGC ATT GAC GTG AAG GAA GTG GAC CCC GCC AGC AAC ACC TAC 249
790 ACC CTT GTC ACC TGC CTG GGC CTT TCC TAT GAT GGC CTG CTG 291
791 GGT AAT AAT CAG ATC TTT CCC AAG ACA GGC CTT CTG ATA ATC 333
792 GTC CTG GGC ACA ATT GCA ATG GAG GGC GAC AGC GCC TCT GAG 375
793 GAG GAA ATC TGG GAG GAG CTG GGT GTG ATG GGG GTG TAT GAT 417
794 GGG AGG GAG CAC ACT GTC TAT GGG GAG CCC AGG AAA CTG CTC 459
795 ACC CAA GAT TGG GTG CAG GAA AAC TAC CTG GAG TAC CGG CAG 501

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796 GTA CCC GGC AGT AAT CCT GCG CGC TAT GAG TTC CTG TGG GGT 543
797 CCA AGG GCT CTG GCT GAA ACC AGC TAT GTG AAA GTC CTG GAG 585
798 CAT GTG GTC AGG GTC AAT GCA AGA GTT CGC ATT GCC TAC CCA 627
799 TCC CTG CGT GAA GCA GCT TTG TTA GAG GAG GAA GAG GGA GTC 669
800 TGAGCATGAG TTGCAGCCAG GGCTGTGGGG AAGGGGCAGG GCTGGGCCAG 719
801 TGCATCTAAC AGCCCTGTGC AGCAGCTTCC CTTGCCTCGT GTAACATGAG 769
802 GCCCATTCTT CACTCTGTTT GAAGAAAATA GTCAGTGTTT TTAGTAGTGG 819
803 GTTTCTATTT TGTGATGA CTTGGAGATT TATCTCTGTT TCCTTTTACA 869
804 ATTGTTGAAA TGTTCCCTTT AATGGATGGT TGAATTAAC TCAGCATCCA 919
805 AGTTTATGAA TCGTAGTTAA CGTATATTGC TGTTAATATA GTTTAGGAGT 969
806 AAGAGTCTTG TTTTATTTC AGATTGGGAA ATCCGTTCTA TTTTGTGAAT 1019
807 TTGGGACATA ATAACAGCAG TGGAGTAAGT ATTTAGAAGT GTGAATTC 1067
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810 (2) INFORMATION FOR SEQUENCE ID NO: 14:
811 (i) SEQUENCE CHARACTERISTICS:
812 (A) LENGTH: 226 base pairs
813 (B) TYPE: nucleic acid
814 (C) STRANDEDNESS: singular
815 (D) TOPOLOGY: linear
816 (ii) MOLECULE TYPE: genomic DNA
817 (ix) FEATURE:
818 (A) NAME/KEY: MAGE-5 gene
819 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:
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823 AGGATCCCCA GGAGGCCCTA GAGGAGCACC AAAGGAGAAG ATCTGTAAGT 50
824 AAGCCTTTGT TAGAGCCTCC AAGGTTTCAGT TTTTAGCTGA GGCTTCTCAC 100
825 ATGCTCCCTC TCTCTCCAGG CCAGTGGGTC TCCATTGCCC AGCTCCTGCC 150
826 CACACTCCTG CCTGTTGCGG TGACCAGAGT CGTC 184
827 ATG TCT CTT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA 226
828

829 (2) INFORMATION FOR SEQUENCE ID NO: 15:
830 (i) SEQUENCE CHARACTERISTICS:
831 (A) LENGTH: 225 base pairs
832 (B) TYPE: nucleic acid
833 (C) STRANDEDNESS: singular
834 (D) TOPOLOGY: linear
835 (ii) MOLECULE TYPE: cDNA
836 (ix) FEATURE:
837 (A) NAME/KEY: MAGE-6 gene
838 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:
839
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842 TAT TTC TTT CCT GTG ATC TTC AGC AAA GCT TCC GAT TCC TTG 42
843 CAG CTG GTC TTT GGC ATC GAG CTG ATG GAA GTG GAC CCC ATC 84
844 GGC CAC GTG TAC ATC TTT GCC ACC TGC CTG GGC CTC TCC TAC 126
845 GAT GGC CTG CTG GGT GAC AAT CAG ATC ATG CCC AGG ACA GGC 168
846 TTC CTG ATA ATC ATC CTG GCC ATA ATC GCA AGA GAG GGC GAC 210
847 TGT GCC CCT GAG GAG 225
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- (2) INFORMATION FOR SEQUENCE ID NO: 16:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 166 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: singular
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: genomic DNA
(ix) FEATURE:
 (A) NAME/KEY: MAGE-7 gene
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

ACA AGC ACT AGT TTC CTT GTG ATC TAT GGC AAA GCC TCA GAG	42
TGC ATG CAG GTG ATG TTT GGC ATT GAC ATG AAG GAA GTG GAC	84
CCC GCG GCC ACT CCT ACG TCT TGT ACC TGC TTG GGC CTC TCC	126
TAC AAT GGC CTG CTG GGT GAT GAT CAG AGC ATG CCC GAG A	166

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/07/807,043A

DATE: 08/31/92
TIME: 14:55:46

LINE ERROR

ORIGINAL TEXT

24 Wrong application Serial Number
410 Entered and Calc. Seq. Length differ

(A) APPLICATION NUMBER: 07/807,043
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8

PAGE: 1

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION US/07/807,043A

DATE: 08/31/92
TIME: 14:55:46

MANDATORY IDENTIFIER THAT WAS NOT FOUND

COUNTRY

LINE ORIGINAL TEXT

CORRECTED TEXT

3 (i) APPLICANTS: Boon, Thierry, Van den
50 (2) INFORMATION FOR SEQUENCE ID NO: 1:
72 (2) INFORMATION FOR SEQUENCE ID NO: 2:
140 (2) INFORMATION FOR SEQUENCE ID NO: 3:
159 (2) INFORMATION FOR SEQUENCE ID NO: 4:
206 (2) INFORMATION FOR SEQUENCE ID NO: 5:
318 (2) INFORMATION FOR SEQUENCE ID NO: 6:
339 (2) INFORMATION FOR SEQUENCE ID NO: 7:
401 (2) INFORMATION FOR SEQUENCE ID NO: 8:
536 (2) INFORMATION FOR SEQUENCE ID NO: 9:
642 (2) INFORMATION FOR SEQUENCE ID NO: 10:
678 (2) INFORMATION FOR SEQUENCE ID NO: 11:
733 (2) INFORMATION FOR SEQUENCE ID NO: 12:
771 (2) INFORMATION FOR SEQUENCE ID NO: 13:
810 (2) INFORMATION FOR SEQUENCE ID NO: 14:
829 (2) INFORMATION FOR SEQUENCE ID NO: 15:
853 (2) INFORMATION FOR SEQUENCE ID NO: 16:

(i) APPLICANT: Boon, Thierry, Van den E
(2) INFORMATION FOR SEQ ID NO: 1:
(2) INFORMATION FOR SEQ ID NO: 2:
(2) INFORMATION FOR SEQ ID NO: 3:
(2) INFORMATION FOR SEQ ID NO: 4:
(2) INFORMATION FOR SEQ ID NO: 5:
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(2) INFORMATION FOR SEQ ID NO: 10:
(2) INFORMATION FOR SEQ ID NO: 11:
(2) INFORMATION FOR SEQ ID NO: 12:
(2) INFORMATION FOR SEQ ID NO: 13:
(2) INFORMATION FOR SEQ ID NO: 14:
(2) INFORMATION FOR SEQ ID NO: 15:
(2) INFORMATION FOR SEQ ID NO: 16: